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IN THE CLAIMS:

Please amend the claims as follows.

Claims 1-34. (Cancelled)

35. (Previously presented) A method to detect expression of a first transgenic

nucleic acid molecule in a sample having either (a) a detectable amount of mRNA tran-

scribed from a second transgenic nucleic acid molecule or (b) a substantially non-detect-

able amount of said mRNA, said method comprising providing a complementary DNA of

the mRNA, amplifying said complementary DNA and hybridizing said complementary

DNA with at least one oligonucleotide designed to hybridize to said second transgenic

nucleic acid molecule whereby said hybridizing indicates the expression of said first

transgenic nucleic acid molecule in a sample.

36. (Previously presented) A method according to claim 35 further comprising

quantitation of mRNA transcribed from said second transgenic nucleic acid molecule.

37. (Previously presented) A method according to claim 35 wherein said second

transgenic nucleic acid molecule which is selected from the group consisting of signal

sequences, 3' UTR sequences and 5' UTR sequences.

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38. (Previously presented) A method according to claim 35 wherein said second

transgenic nucleic acid molecule is a 3' untranslated sequence from the 3' end of the

Pisum sativum rbcS E9 gene.

39. (Previously presented) A method according to claim 35 wherein said second

transgenic nucleic acid molecule has a sequence of SEQ ID NO: 2.

40. (Previously presented) A method according to claim 35 wherein the at least

one oligonucleotide is a sequence which is a molecule selected from the group consisting

of SEQ ID NO: 7 SEQ ID NO: 8, SEQ ID NO: 9 and SEQ ID NO: 28.

41. (Previously presented) A method according to claim 35 wherein the amplify-

ing is carried out by a method selected from the group consisting of PCR or RT-PCR.

42. (Previously presented) A method according to claim 36 wherein the quanti-

tation of mRNA is determined by a method selected from the group consisting of quanti-

tative RT-PCR or competitive quantitative RT-PCR.

43. (Previously presented) A method according to claim 35 wherein said second

transgenic nucleic acid molecule comprises at least 100 base pairs of consecutive se-

quence having a sequence of SEQ ID NO: 2.

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44. (Previously presented) A method according to claim 35 wherein at least one

oligonucleotide comprises at least 15 bases from or complementary to a consecutive se-

quence of SEQ ID NO: 2.

45. (Previously presented) A method according to claim 35 wherein at least one

oligonucleotide has a detectable label.

46. (Previously presented) A method according to claim 45 wherein said label is

selected from the group consisting of a fluorescent label, a digoxigenen-dUTP label, a

biotin label, and a radiolabel.

47. (Previously presented) A method according to claim 35 wherein said at least

one oligonucleotide comprises a pair of oligonucleotide primers and an oligonucleotide

probe designed to hybridize to said second transgenic nucleic acid molecule in a 5' nu-

clease assay.

48. (Previously presented) A method according to claim 47 wherein each of said

primer pair used in said amplification comprises 15 to 30 bases identical or comple-

mentary to a consecutive sequence of a second transgenic nucleic acid molecule having a

sequence selected from the group consisting of signal sequences, 3' UTR sequences and

5' UTR sequences and wherein said probe comprises 15 to 30 bases complementary or

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identical to a second transgenic nucleic acid molecule having a sequence selected from

the group consisting of signal sequences, 3' UTR sequences and 5' UTR sequences.

49. (Previously presented) A method according to claim 35 further comprising

Southern Blotting, Northern Blotting or RNAse protection assay.

50. (Currently amended) An amplification kit for the detection of a transgenic

nucleic acid molecule comprising at least one primer pair and a corresponding labeled

probe which hybridizes under stringent hybridization conditions to a nucleic acid mole-

cule of a 3' untranslated sequence of a 3' end of the Pisum sativum rbcS E9 gene.

51. (New) A method to detect expression of a first transgenic nucleic acid mole-

cule in a sample having either (a) a detectable amount of mRNA transcribed from a sec-

ond transgenic nucleic acid molecule or (b) a substantially non-detectable amount of said

mRNA, said method comprising providing a complementary DNA of the mRNA, ampli-

fying said complementary DNA and hybridizing said complementary DNA with at least

one oligonucleotide designed to hybridize to said second transgenic nucleic acid mole-

cule whereby said hybridizing indicates the expression of said first transgenic nucleic

acid molecule in a sample and wherein said at least one oligonucleotide is a sequence

which is a molecule selected from the group consisting of SEQ ID NO: 7 SEQ ID NO: 8,

SEQ ID NO: 9 and SEQ ID NO: 28.

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52. (New) A method to detect expression of a first transgenic nucleic acid mole-

cule in a sample having either (a) a detectable amount of mRNA transcribed from a sec-

ond transgenic nucleic acid molecule or (b) a substantially non-detectable amount of said

mRNA, said method comprising providing a complementary DNA of the mRNA, ampli-

fying said complementary DNA and hybridizing said complementary DNA with at least

one oligonucleotide designed to hybridize to said second transgenic nucleic acid mole-

cule whereby said hybridizing indicates the expression of said first transgenic nucleic

acid molecule in a sample and wherein said second transgenic nucleic acid molecule is

the sequence of SEQ ID NO: 2.